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L3: Entry 1 of 19 File: USPT Jul 10, 2001

DOCUMENT-IDENTIFIER: US 6258264 B1
TITLE: Non-polar media for polynucleotide separations

DEPR:
Unlike capillary electrophoresis (CE), PCR samples do not have to be desalted prior to analysis by MIPC. This represents a decisive advantage of MIPC over CE. With MIPC, it is thus possible to achieve a fully automated analysis of PCR samples if an automatic autosampler is utilized. Moreover, since the volume of sample injection is known, in contrast to CE, quantitation over several orders of magnitude can be achieved without the need for an internal standard, hence allowing the quantitation of gene expression, as well as the determination of virus titers in tissues and body fluids. A fully automated version of the method of the invention can be used to discriminate (distinguish) normal from mutated genes, as well as to detect oncogenes, bacterial and viral genome polynucleotides (hepatitis C virus, HIV, tuberculosis) for diagnostic purposes. Moreover, adjustment of column temperature allows one to moderate the stringency of hybridization reactions or to separate heteroduplex from homoduplex DNA species.

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L3: Entry 10 of 19 File: USPT Feb 22, 2000

DOCUMENT-IDENTIFIER: US 6027880 A
TITLE: Arrays of nucleic acid probes and methods of using the same for detecting cystic fibrosis

DEPR:
A particular advantage of the present sequencing strategy over conventional sequencing methods is the capacity simultaneously to detect and quantify proportions of multiple target sequences. Such capacity is valuable, e.g., for diagnosis of patients who are heterozygous with respect to a gene or who are infected with a virus, such as HIV, which is usually present in several polymorphic forms. Such capacity is also useful in analyzing targets from biopsies of tumor cells and surrounding tissues. The presence of multiple target sequences is detected from the relative signals of the four probes at the array columns corresponding to the target nucleotides at which diversity occurs. The relative signals of the four probes for the mixture under test are compared with the corresponding signals from a homogeneous reference sequence. An increase in a signal from a probe that is mismatched with respect to the reference sequence, and a corresponding decrease in the signal from the probe which is matched with the reference sequence, signal the presence of a mutant strain in the mixture. The extent in shift in hybridization signals of the probes is related to the proportion of a target sequence in the mixture. Shifts in relative hybridization signals can be quantitatively related to proportions of reference and mutant sequence by prior calibration of the chip with seeded mixtures of the mutant and reference sequences. By this means, a chip can be used to detect variant or mutant strains constituting as little as 1, 5, 20, or 25% of a mixture of stains.

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Search History

Today's Date: 10/22/2001

DB Name	Query	Hit Count	Set Name
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USPT	l1 same detect$ same hybridiz$	44	L2
USPT	muta$ same HIV	1624	L1

(FILE 'HOME' ENTERED AT 13:46:18 ON 22 OCT 2001)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE' ENTERED AT 13:46:34 ON 22 OCT 2001

L1 506 S (REDUC? OR DECREAS?) (P) (BACKGROUND (W) SIGNAL?)

L2 1 S L1 (P)HYBRIDIZ? (P)PROBE? (P)MISMATCH?

L2 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2001 ACS
AN 2001:654744 CAPLUS
DN 135:222328
TI Use of deliberately-introduced mismatch to minimize background in nucleic acid hybridization
IN De Baar, Marinus Petrus; Van Gemen, Bob; Timmermans, Eveline Catherina Anna Clasina
PA Amsterdam Support Diagnostics B.V., Neth.
SO Eur. Pat. Appl., 14 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 1130119	A1	20010905	EP 2001-1200532	20010215
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
PRAI	EP 2000-200549	A	20000217		

AB The invention provides a method for **reducing** background in **hybridization** reactions of nucleic acids involving at least two homologous **probes**, wherein at least one of said **probes** is non-linear, or two homologous target sequences and a non-linear, e.g. loop-forming, **probe** such as a beacon **probe**. Background is **reduced** by introducing an intended **mismatch** with a target sequence in at least one of said **probes**. The presence of the **mismatch reduces** the specificity of **probes** not entirely complementary to a target sequence to such an extent that the **background signal** is **reduced**. A set of mixed homologous **probes**, wherein at least one of said **probes** is non-linear, comprising such specific **mismatch** is also provided. Said set can be used for the detection of variants of a family of nucleic acids, for instance a no. of HIV variants. The invention also provides kits for carrying out the methods according to the invention.

RE.CNT 7
RE
(1) de Baar, M; JOURNAL OF CLINICAL MICROBIOLOGY 2001, V39(5), P1895 CAPLUS
(2) Didenko, V; BIOTECHNIQUES 1999, V27(6), P1130 CAPLUS
(3) Guo, Z; NATURE BIOTECHNOLOGY 1997, V15, P331 CAPLUS
(4) Leone; NUCLEIC ACIDS RESEARCH 1998, V26(9), P2150 CAPLUS
(5) Marras, S; GENETIC ANALYSIS: BIOMOLECULAR ENGINEERING 1999, V14(5-6), P151 CAPLUS
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